UNITED STATES DISTRICT COURT
WESTERN DISTRICT OF MICHIGAN
SOUTHERN DIVISION

UNITED STATES OF AMERICA,

Plaintiff,

v.

No. 17-cr-130

DANIEL GISSANTANER,

HON. JANET T. NEFF
United States District Judge

Defendant.
_____/

UNITED STATES' BRIEF IN OPPOSITION TO DEFENDANT'S MOTION TO EXCLUDE DNA ANALYSIS

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The defendant has moved to exclude the DNA analysis conducted by the Michigan State Police ("MSP") on swabs collected from the defendant and from a firearm seized from the defendant's home. The MSP analysis concluded that the DNA profile on the swab from the firearm was 49 million times more likely to be found if it contained the defendant's DNA than if it did not. Recognizing the significance of this evidence to the government's case, the defendant adopts a kitchen-sink approach to attempt to keep the evidence from the jury, arguing that the Battle Creek Police Department ("BCPD") mishandled the evidence, that the MSP laboratory did not use the analysis software, STRmix, properly, that the software is not a reliable tool for determining likelihood ratios, and that likelihood ratios themselves are improper. None of these arguments warrants exclusion of the evidence.

I. FACTUAL BACKGROUND

On September 25, 2015, officers from the BCPD responded to a 911 call in which the caller reported a man with a gun. The officers eventually determined the caller was a woman, Lisa Harvey, whose boyfriend, Gary Rose, was in the process of moving in with her. Gissantaner, the couple's neighbor, and Rose had had an altercation about the location of Rose's trailer on a shared driveway. In his initial statement to the police, Rose said that during the argument Gissantaner said something like, "I've got something for you," entered his house, came back out, and pulled a "dark object" from his waistband. Rose reported that because it was nighttime, he could not tell exactly what the object was, but he thought it was a gun. Rose later said that he saw Gissantaner pointing a gun at him.

The police interviewed one of Gissantaner's roommates, Cory Patton, who was, like Gissantaner, also a convicted felon. In his initial statement, Patton said that he heard a fight, went outside, and took the gun away from Gissantaner. He later said that he never saw

Gissantaner with the gun, but he heard a fight, and then found a gun he had never seen before on their shared kitchen counter. Patton consented to a search of a chest in his bedroom, where police seized the gun in question. Patton indicated he put the gun there for safekeeping because children lived in the home.

The police swabbed the gun and Gissantaner for DNA and submitted the samples to a lab for comparison. The lab concluded that the swab from the gun contained a mixture of DNA, and, using the STRmix software package, determined that there was "very strong support that Daniel Gissantaner is a contributor to the DNA profile developed from the swab from" the gun, (formally, the lab concluded "it is at least 49 Million times more likely if the observed DNA profile from the swabs of textured areas of GUN-001 originated from Daniel Gissantaner and two unrelated, unknown contributors than if the data originated from three unrelated, unknown individuals"). (PageID.920.)

A federal grand jury indicted the defendant for being a felon in possession of a firearm, and this motion followed.

II. LEGAL STANDARD

In *Daubert v. Merrell Dow Pharmaceuticals*, 509 U.S. 579 (1993), the Supreme Court enunciated the framework to be used by district courts in performing the gatekeeping function of protecting the jury from junk science. "[U]nder the [Federal Rules of Evidence] the trial judge must ensure that any and all scientific testimony or evidence admitted is not only relevant, but reliable." *Id.* at 589. *Daubert* teaches that the trial judge must first ensure that the testimony encompasses "'scientific knowledge'" that is "supported by appropriate validation—*i.e.*, 'good grounds,' based on what is known." *Id.* at 590. Second, "the evidence or testimony [must]

'assist the trier of fact to understand the evidence or to determine a fact in issue.'" *Id.* at 591 (quoting Fed. R. Evid. 702).

The Supreme Court outlined some of the "factors [that] bear on the inquiry," carefully noting that the Court did "not presume to set out a definitive checklist or test." *Id.* at 593. First, the trial court should examine "whether a theory or technique . . . can be (and has been) tested." *Id.* Second, the court reviews whether it "has been subjected to peer review and publication." *Id.* Third, the court should discern "the known or potential rate of error and the existence and maintenance of standards controlling the technique's operation." *Id.* at 594 (citation omitted). Finally, the trial judge should consider the old standard under *Frye v. United States*, 293 F. 1013 (1923), "general acceptance" within the scientific community. *See id.* The *Daubert* factors can "be tailored to the facts of a particular case" and are not always dispositive, because the inquiry is flexible. *In re Scrap Metal Antitrust Litig.*, 527 F.3d 517, 529 (6th Cir. 2008).

III. ARGUMENT

Gissantaner's attacks on the DNA evidence can be separated into two groups: those directed to the scientific analysis in the case—both theoretical, and as applied—and those alleging police incompetence and implying malfeasance. Both groups of arguments fail to justify exclusion of the evidence, and the latter set are premature, as they are for the jury.

A. STRmix Is a Valid Tool for Analyzing Mixtures of DNA and Was Used Properly in this Case

Probabilistic genotyping in general, and STRmix in particular, represent a significant development in forensic science because STRmix allows for the calculation of a likelihood ratio for a specific defendant's DNA being in a mixture, a complicated mathematical problem that was not practically solvable until earlier this decade. In that sense it is new. But, as with almost all scientific developments, it is not a watershed theory or entirely novel concept. *See generally*

Thomas S. Kuhn, *The Structure of Scientific Revolutions* (2d ed. 1962) (excerpt attached as Ex. 1)[1] (explaining that science usually progresses during normal, puzzle-solving phases, rarely interrupted by a revolutionary phase). Instead, it is built on established mathematical, chemical, and genetic principles, and combines those principles in such a way to achieve something that was previously unachievable. In that sense there is nothing new about it at all.

1. Probabilistic Genotyping Is an Interdisciplinary Application of Advanced Statistical Methods to Population Genetics

As even Gissantaner acknowledges, traditional forensic DNA analysis has been accepted as reliable in federal courtrooms for at least twenty-five years. The power of forensic DNA comparison is ubiquitous to the point where it has infiltrated popular culture. In large part that power is attributable to statistics; it is highly improbable to find two individuals with the same genetic profile, unless they are identical twins. That improbability is often expressed as a likelihood ratio, which is simply the relative likelihoods of two mutually exclusive hypotheses (for example, Gissantaner was a contributor to the DNA mixture found on the gun, and Gissantaner was not a contributor).[2]

Forensic DNA comparison does not analyze a person's entire genome, which comprises three billion base pairs, in part because the labor associated with whole genome sequencing has been historically cost-prohibitive and is ultimately unnecessary. By comparing small, agreed upon regions of the genome, forensic scientists are able to determine likelihood ratios that are sufficiently high such that all reasonable people would agree that the samples for comparison are

[1] The government has attached to its briefs those exhibits not readily accessible via a legal database such as Westlaw or via the internet.

[2] Likelihood ratios are used not only for forensic analysis in criminal investigations, but also in paternity index calculations. Another common statistic used in forensic DNA analysis is the random match probability, which is a type of likelihood ratio (although a likelihood ratio is not necessarily a random match probability).

a "match." *See, e.g.*, Michael J. Saks et al., *Reference Guide on DNA Evidence*, *Reference Manual on Scientific Evidence* 491 (Federal Judicial Center, 2d ed. 2000). The small, agreed upon regions of the genome used most often today are called short tandem repeats, or "STRs." The region at which a particular STR is found is called a locus. The particular gene that an individual has at a locus—in the case of STRs, a specific number of repeats—is called an allele. STRs are useful features for comparison because while every person has STRs at the loci, there is variation in the number of repeats in a given STR for each person (that is, different people can have different alleles), and the range of variation is known by population studies. *See id.* at 495–98.

For example, one locus used in forensic STR analysis is D7S820. At that locus, the STR is GATA, a representational acronym for the bases guanine, adenine, thymine, and adenine again. Humans have from anywhere between five and sixteen repeats of the GATA STR on each chromosome. *See* National Institute of Standards and Technology ("NIST"), STRBase, D7S820, http://strbase.nist.gov/str_D7S820.htm (last visited Feb. 14, 2018). Gissantaner's allele has ten repeats, and only ten repeats, meaning both his mother and father contributed the same allele to him. (*See* Ex. 2: STRmix Electropherogram, at 1.)

Given the natural variation of repeats at each STR locus, by looking at a sufficiently large number of loci, it is highly improbable that any two people who are not identical twins would have the exact same profile. The FBI at one point used thirteen core loci, and in 2017 increased that number to twenty. FBI, Combined DNA Index System, https://www.fbi.gov/services/laboratory/biometric-analysis/codis (last visited Feb. 14, 2018); NIST, FBI CODIS Core STR Loci, http://strbase.nist.gov/fbicore.htm. The MSP laboratory attempts amplification of STRs at 24 loci. (PageID.957.) The relative likelihood between the

unknown evidentiary sample's DNA matching the known defendant's reference sample because they are one and the same, and simply matching it by chance, is expressed as a likelihood ratio. *See, e.g.*, Saks, *supra*, at 520–37.

Each of a person's twenty-three pairs of chromosomes comprise one chromosome from the mother, and one from the father. Therefore, at each locus, where only one DNA profile is found on the evidentiary sample, an analyst would expect to see either one or two signal peaks.[3] (As with Gissantaner's D7S820 locus, where both chromosomes have the same number of repeats, only one peak will show.) Where, however, three or more called peaks appear at a locus, the analyst knows the unknown profile usually contains a mixture of DNA.

What is at issue in Gissantaner's motion is not the reliability of the chemical process that leads to the electropherogram. He cannot and does not seriously dispute DNA extraction, or PCR amplification, or capillary electrophoresis—all processes that were accepted as reliable components of DNA analysis a long time ago.[4] *See, e.g.*, Saks, *supra*, at 497–500. Instead, he

[3] The "peaks" are found on electropherograms, which are the output of a process called capillary electrophoresis. Though not at issue in this motion (save for undeveloped and incredible arguments raised by Gissantaner that are addressed in footnote 4 below), the process for obtaining a DNA profile for analysis begins with taking a swab from the source. The swab is dissolved in a buffer, and then the cells are lysed and the DNA released into solution. Prefabricated primers (molecules that are a series of bases used to prime the right loci for amplification) are added to the solution, and a polymerase chain reaction leads to the replication, or amplification, of the loci containing the STRs. The length of each STR is then measured based on the distance it travels in the capillary under an electric field, and the resulting read-out shows the peaks in the electropherogram. Either an analyst, or the software, can "call" peaks to differentiate signal from noise. Noise, by way of example, can come from artifacts of the PCR process that result in small peaks not indicative of actual alleles. (PageID.940–41, 951–67.) *See* Saks, *supra*, at 497–99, 563–66.

[4] Gissantaner takes passing shots at a few biological and chemical aspects of DNA analysis that have long been accepted. Gissantaner criticizes capillary electrophoresis as "an automated process using a genetic analyzer that does not involve first-hand visual interpretation," unlike the gel electrophoresis used in *United States v. Bonds*, 12 F.3d 540 (6th Cir. 1993), and he likewise goes after PCR amplification. (PageID.768.) But Gissantaner uses *Bonds* as a straw man. Aside from its general recognition of the validity of DNA analysis, the

contests only the interpretation of the output of those chemical processes using probabilistic genotyping and STRmix.

The math to determine the likelihood ratio is more involved when the unknown sample contains more alleles than can be explained by a single contributor. But longstanding mathematical tools are available to solve that math problem. Probabilistic genotyping employs the Monte Carlo statistical method to derive a likelihood ratio that describes the comparative likelihoods of the reference sample being contained in the mixture and the profile of the reference sample appearing in the mixture by chance. *See* STRmix, https://strmix.esr.cri.nz (last visited Feb. 14, 2018) ("A range of Likelihood Ratio options are provided for subsequent comparisons to reference profiles. Using a Markov Chain Monte Carlo engine, STRmix™ models allelic and stutter peak heights (both back and forward stutter) as well as drop-in and

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extended discussion of *Bonds* is inapt because of the tremendous advancement in DNA analysis in the 25 years since that case was decided and relatedly because the method of analysis at issue in this case is concededly different than that reviewed by the Sixth Circuit in *Bonds*. (PageID.768–69.) Gissantaner's undeveloped remarks denigrating PCR amplification and capillary electrophoresis—in short that seeing is believing and the technology is not to be trusted because it cannot be visually seen—misses the mark. The argument is absurd precisely because of the scientific advancements that followed *Bonds*. It is akin to criticizing smartphones as compared to rotary phones because the numbers cannot be felt as they are dialed. Capillary electrophoresis is a faster, more accurate version of its gel predecessors. *See, e.g.*, Saks, *supra*, at 566 ("[C]apillary electrophoresis . . . . is faster and uses smaller samples than gel electrophoresis, and it can be automated."). And PCR amplification is used every day in academic settings around the world. *See id.* at 500 ("[T]he existence of PCR-based procedures that can ascertain genotypes accurately cannot be doubted."); Wikipedia, Polymerase chain reaction, https://en.wikipedia.org/wiki/Polymerase_chain_reaction (last visited Feb. 14, 2018) ("PCR is now a common and often indispensable technique used in clinical and research laboratories for a broad variety of applications."). In the same vein of these anachronistic swipes at DNA technology, Gissantaner's antiscientific knock on the cellular source of DNA—it seems he favors blood over epithelial cells, (PageID.768)—likewise is misplaced, because each cell type contains an identical copy of a person's DNA, with some exceptions not relevant here. *See, e.g.*, National Institute of Health, National Human Genome Research Institute, 2009 National DNA Day Online Chatroom Transcript, Question 153, https://www.genome.gov/dnaday/q.cfm?aid=153&year=2009 (last visited Feb. 14, 2018) (answering a question from a ninth-grade student by stating in part, "All the cells in a person's body have the same DNA and the same genes.").

drop out behaviour. . . . STRmix™ is supported by comprehensive empirical studies with its mathematics readily accessible to DNA analysts, so results are easily explained in court.").

In short, probabilistic genotyping is an application of established principles in a new way. For that reason, it should readily survive Gissantaner's challenge.

2. STRmix Reliably Implements Probabilistic Genotyping

Gissantaner also attacks STRmix's implementation of probabilistic genotyping. Even if probabilistic genotyping is an acceptable methodology, the argument goes, STRmix does not use the discipline correctly. (*See* PageID.767.) This argument is simply wrong.

First, STRmix was developed by experts in probabilistic genotyping, and tested by them extensively. STRmix has been studied in academic literature. This is all evidence of STRmix's reliability "external" to its application by the MSP. STRmix, https://strmix.esr.cri.nz (last visited Feb. 14, 2018) (collecting nineteen publications from 2013 to 2017 that "describ[e] the biological model, mathematics, performance and validation for STRmix[]"); *see* STRmix Validations, https://johnbuckleton.wordpress.com/strmix/strmix-validations/ (last visited Feb. 14, 2018) (collecting publicly available laboratory validations, including from the District of Columbia, New York, and San Diego crime labs); Jo-Anne Bright et al., *Internal validation of STRmix™ – A multi laboratory response to PCAST*, 34 Forensic Science International: Genetics 11–24 (2018) (attached as Ex. 3) ("We report a large compilation of the internal validations of the probabilistic genotyping software STRmix™. Thirty one laboratories contributed data resulting in 2825 mixtures comprising three to six donors and a wide range of multiplex, equipment, mixture proportions and templates."); Tamyra R. Moretti et al., *Internal validation of STRmix™ for the interpretation of single source and mixed DNA profiles*, 29 Forensic Science

International: Genetics 126–44 (2017) (attached as Ex. 4) (publishing the FBI's internal validation of STRmix).

Next, the MSP laboratory tested STRmix's reliability internally with known samples and found it valid before it began using the program to analyze new samples. Internal validation is an important check on the reliability of any new forensic tool to be sure that it can be implemented correctly using the tools already available in the particular laboratory. The report of MSP's internal validation was filed by Gissantaner as Attachment 14 to his brief. (PageID.1014–61.) The government is prepared to call at any evidentiary hearing the MSP personnel who oversaw the validation process for STRmix. The MSP validation relied in part on guidelines from a national working group. (PageID.1016, 1031, 1061.) *See generally* Scientific Working Group on DNA Analysis Methods ("SWGDAM"), *Guidelines for the Validation of Probabilistic Genotyping Systems* (June 15, 2015), https://www.swgdam.org/publications (last visited Feb. 14, 2018).

In addition to the published materials validating STRmix, MSP's internal validation is sufficient for purposes of *Daubert*. Validation is the means by which the laboratory tests a product to establish that it functions as expected. *See Williams v. Illinois*, 567 U.S. 50, 95 (2012) (Breyer, J., concurring) (observing that forensic DNA laboratories that seek to "access the FBI's Combined DNA Index System [CODIS] must adhere to standards governing, among other things . . . validation of testing methodologies"). By analogy, a driver who tests a car by driving it hundreds of miles can testify that the car does what the manufacturer says it does, even if the driver does not understand how the engine works. Here, prior to adopting STRmix, the MSP laboratory tested it on known mixtures of DNA to determine whether it could accurately do what the developers said it could do. That it passed internal validation, combined with the peer review

and external validation, is sufficient to meet the *Daubert* requirements. Two federal courts have admitted STRmix analyses based on internal validation studies. *See United States v. Russell*, No. 1:14-cr-02563-MCA, slip op. at 16–17 (D.N.M. Jan. 10, 2018) (attached as Ex. 5) (explaining that the court reviewed the "developmental and internal validation study papers," which complied with the SWGDAM guidelines (footnote omitted)); *United States v. Pettway*, No. 12-CR-103, 2016 WL 6134493, at *1 (W.D.N.Y. Oct. 21, 2016) (admitting STRmix evidence in part due to "internal validation studies" from which it was "concluded that STRmix provides consistently accurate information").

Because internal validation is sufficient to satisfy *Daubert*, Gissantaner is wrong that he has a constitutional right to "confront[]" the developer of the software. (PageID.767.) The Confrontation Clause does not apply to *Daubert* hearings. *See United States v. Karmue*, 841 F.3d 24, 26–27 (1st Cir. 2016) (observing that the confrontation right has never been extended beyond trial but leaving open the possibility it could apply to a *Daubert* hearing, though avoiding the question by finding any error harmless); *United States v. Aguilera-Meza*, 329 F. App'x 825, 833 (10th Cir. 2009) (finding no confrontation violation where the district court declined to hold a *Daubert* hearing); *see also United States v. Mitchell-Hunter*, 663 F.3d 45, 51–52 (1st Cir. 2011) (collecting cases) ("Mitchell does not point to a single case extending the right to confrontation beyond the context of trial, although there is extensive case law declining to apply the confrontation right to various pre- and post-trial proceedings."). Gissantaner's confrontation argument is limitless to the point of impossibility: as all forensic evidence is built on a vast number of individual scientific ideas, application of the confrontation right would allow a criminal defendant to turn each and every case in which forensic evidence is used into an endless parade of scientific experts. What Gissantaner further ignores, moreover, is that he also has the

ability to bring witnesses to any *Daubert* hearing, meaning he has no grounds to complain about the violation of the Confrontation Clause based on the government's chosen witnesses. *See United States v. Adams*, 189 F. App'x 120, 124 (3d Cir. 2006) ("[B]ecause appellants fail to show (or even argue) that they were somehow prevented from calling these 'actual' witnesses themselves, their reliance on *Crawford* is untenable. Appellants were able to cross-examine the government's expert witness at trial, and if they wanted to question those who actually performed the tests on the masks, they should have called those individuals as witnesses.").

Lastly, Gissantaner contends that STRmix is unreliable because it does not return identical results each time it is run. (PageID.752, 765.) This argument ignores a deeper truth about science: all measurement is subject to variability. Even when drugs are weighed by federal laboratories, their reports express the drug weight—mass—as subject to a confidence interval that documents uncertainty in the weight. That does not mean the scales are unreliable, but rather that while we can have a high degree of confidence in the approximate weight, we have a lower degree of confidence in the precise weight. The same principle applies to the complex statistical algorithm used by STRmix: there is little uncertainty in the conclusions derived from its use, even if there is some inevitable uncertainty in the precise results from a single calculation.[5]

3. The PCAST Report Is Misinterpreted and the Article by NIST Employees Is Wrong

Looking to appeal to governmental authority, Gissantaner attacks probabilistic genotyping and STRmix by misreading a report issued by the President's Council of Advisors on

[5] The source code for STRmix can be made available to defense counsel upon request. *See* ESR, Access to STRmix™ Software by Defence Legal teams, https://strmix.esr.cri.nz/assets/Uploads/Defence-Access-to-STRmix-April-2016.pdf (last visited Feb. 14, 2018).

Science and Technology ("2016 PCAST Report"). (PageID.760–63.) Curiously, Gissantaner submits that the 2016 PCAST Report supports his position, while acknowledging that the report observes that "[t]hese probabilistic genotyping software programs" are "a major improvement" in analyzing DNA mixtures. (PageID.762, 1174.) Presumably Gissantaner thinks the report is an asset because of the unremarkable proposition that new software programs "require careful scrutiny" to make sure they do what they say they do. (*Id.*) He also believes that because there is some evidence that Gissantaner was a minor contributor with a contribution to the mixture of less than 20%, and further because he claims the mixture may have had four contributors, the report's assertion that STRmix and a competitor, TrueAllele, "appear to be reliable for three-person mixtures in which the minor contributor constitutes at least 20 percent of the intact DNA" means STRmix could not have been used properly in this case. (PageID.762, 1175.)

As to the first point, the 2016 PCAST Report is unhelpful to Gissantaner because it largely endorses probabilistic genotyping and STRmix, as noted in the passages quoted above. The addendum to the 2016 PCAST Report observed that after meeting with the software's developer, Dr. John Buckleton, both Dr. Buckleton and PCAST agreed that empirical validation on different samples was an appropriate means to test the software. 2016 PCAST Report Addendum, at 9 (Jan. 6, 2017) (attached as Ex. 6).[6] As discussed above, that empirical validation has been done by forensic laboratories around the world as the use of STRmix

[6] The Addendum goes on to state: "When considering the admissibility of testimony about complex mixtures (or complex samples), judges should ascertain whether the published validation studies adequately address the nature of the sample being analyzed (e.g., DNA quantity and quality, number of contributors, and mixture proportion for the person of interest)." 2016 PCAST Report Addendum, at 9. Dr. Buckleton has thoughtfully pointed out in response that journals are unlikely to publish internal validation studies because they are not novel, but many such studies have been done. *See* https://johnbuckleton.wordpress.com/pcast/ (last visited Feb. 14, 2018) (collecting validation studies). Moreover, as cited above, several such studies have been published.

becomes more and more widespread. *See* https://johnbuckleton.wordpress.com/strmix/ (last visited Feb. 14, 2018) (observing that STRmix "is currently in use in 30 labs in the US, all 8 State and territory labs in Australasia, and 4 labs elsewhere" and attaching a list of active labs, including the FBI, the United States Army, and state labs in Michigan, California, Idaho, Texas, Oregon, Wyoming, Connecticut, Florida, and Indiana).

Nor is the 20-percent threshold and three-person-mixture limitation espoused by PCAST any cause for concern here. Gissantaner contends that he likely contributed only 7% to the DNA mixture according to STRmix, and since 7% is less than 20%, STRmix should not have been used to analyze his sample. (PageID.766–67.). Even assuming he is correct that he is the 7% contributor, PCAST does not control the detection limit of the MSP lab; MSP's internal validation studies do. *See Russell*, No. 1:14-cr-02563-MCA, slip op. at 17 (citing testimony from the expert "that the proportion of DNA from major and minor contributors found in this case was included within the ranges studied in the internal validation study"). And STRmix was validated by the MSP lab for minor contributors below 7%, and for mixtures involving four people. (PageID.1048–50 (demonstrating satisfactory validation for approximate 4% contributor in a four-person mixture). PCAST criticized certain forensic disciplines in lacking uniformity in approach, but tools like STRmix in fact provide uniformity.[7]

[7] Although the government prefers to focus on the scientific merits of the academic discussion in the 2016 PCAST Report, it bears mention that that report has received substantial criticism from forensic scientists. *See, e.g.*, I.W. Evett et al., *Finding the way forward for forensic science in the US—A commentary on the PCAST report*, 278 Forensic Science International 16–23 (2017) (attached as Ex. 7). Indeed, the Department of Justice has rejected the report since it was issued, even under President Obama, whose advisors wrote the report. *See, e.g.*, Gary Fields, Wall Street Journal, Sept. 20, 2016 (quoting Attorney General Loretta Lynch), https://www.wsj.com/articles/white-house-advisory-council-releases-report-critical-of-forensics-used-in-criminal-trials-1474394743 (attached as Ex. 8).

Gissantaner also attacks the use of likelihood ratios themselves, citing one paper written by two employees of NIST that criticizes their use. There are two reasons to reject this claim. First, likelihood ratios have long been used in courtrooms to describe the conclusions of DNA analysis. *See* Saks, *supra*, at 534–37; *see also, e.g.*, *United States v. Williams*, No. CR 05-920-RSWL, 2008 WL 5382264, at *17 (C.D. Cal. Dec. 23, 2008) ("The likelihood ratio approach or a random match probability approach are often used in probable cause cases, in which DNA from a crime scene is compared directly to the DNA profile of a *known* suspect."). Second, respected scientists disagree with the paper cited by the defendant. *See, e.g.*, Geoffrey Stewart Morrison, *A Response to: "NIST experts urge caution in use of courtroom evidence presentation method,"* http://forensic-evaluation.net/NIST_press_release_2017_10/ (last visited Feb. 14, 2018) (explaining the shortcomings of the Lund and Iyer argument). A formal rebuttal of the paper is beyond the scope of this response, but in short, that paper (1) ignores that juries are presumed able to sort through evidence, aided by adversarial examination of the bases of expert opinions, (2) fails to recognize the uncertainty described by the likelihood ratio itself, and (3) is not tailored to analyzing DNA, which among forensic disciplines is comparatively robust insofar as the statistical distribution of alleles in populations have been thoroughly studied and the method for calculating the likelihood ratio carefully honed. The government expects that a formal response to their argument, which itself was published just four months ago, will be published in the coming months.

Gissantaner makes the related argument, based on Rules 401 and 403, that likelihood ratios "would only marginally help the trier of fact to understand the evidence." (PageID.769.) The likelihood ratio is a powerful tool for conveying the probative value of DNA evidence to the jury, and because likelihood ratios are delivered with explanations of their scientific meaning by

qualified experts, there is little risk of confusion. If defense counsel believes that the expert has not properly qualified the explanation, the meaning of the likelihood ratio can be explored on cross examination. *See, e.g.*, *United States v. Stafford*, 721 F.3d 380, 393–95 (6th Cir. 2013) (affirming admission of expert testimony on gun-shot residue because the issue was one of weight and not admissibility and could be challenged through cross examination); *Bonds*, 12 F.3d at 562–63 (admitting DNA evidence and explaining that criticisms of a qualified expert's conclusions or allegations that a lab made a mistake are issues of weight to be explored on cross examination). Gissantaner's claim that cross examination and clear presentation on this issue are "impossible," (PageID.770), is an affront to the jury's essential role in our criminal justice system. *See, e.g.*, *United States v. Harper*, 466 F.3d 634, 647 (8th Cir. 2006) ("[W]e presume juries to be composed of prudent, intelligent individuals . . . ."); *United States v. Williams*, 858 F.2d 1218, 1225 (7th Cir. 1988) ("Juries . . . are presumed capable of sorting through the evidence . . . .").

4. The MSP Used STRmix Correctly

The final set of Gissantaner's arguments directed toward STRmix focus on how the software was used by the MSP lab in his case. He challenges the peak calls made by the analyst in determining that there were only three contributors to the mix, and in disregarding one locus for purposes of calculating the likelihood ratio. Both decisions were sound exercises of the analyst's scientific discretion. Moreover, the analyst's report notes the lab's willingness to conduct calculations using different decisions upon request; Gissantaner has yet to request such analysis by the lab. (PageID.920 ("The propositions were formed from the information available to the undersigned at the time of analysis. If this information changes or other propositions should be considered, the analyst is able to undertake them if instructed with sufficient time.").)

As an initial matter, Gissantaner has attached the wrong set of electropherograms to his motion, although he refers in his brief to comments made by the analyst on the pertinent set. (*Compare* Ex. 2 *with* PageID.1002–13.) The MSP's workflow in this case involved first a forensic scientist not trained in STRmix. That scientist took the first look at the electropherogram of the sample from the gun, determined it was a mixture, and issued the second lab report, simply stating that further analysis was required (because she was not trained to analyze it). The next scientist then stepped in to use STRmix. In order to analyze the electropherograms using STRmix, she had to turn the "stutter filter" off, a required step in MSP's protocol for using STRmix, as documented in Gissantaner's Attachment 12, the MSP's policy manual. (PageID.989 ("The analysis method incorporates the same thresholds and methods as used previously, except the stutter thresholds are removed for the STRMix Casework method.").) The stutter filter is the component of the Applied Biosystems GeneMapper software (used by the MSP to create electropherograms) that calls alleles after capillary electrophoresis is complete (in other words, as discussed above, it differentiates signal from noise). This second set of electropherograms, attached as Exhibit 2 to this brief, documents the STRmix-trained analyst's work in this case.

As Gissantaner observes, the analyst noted on the electropherogram, as she is required to, that the locus D8S1179 was ignored because of the "exhibited oversaturation." According to MSP policy, oversaturated loci can be ignored as inconclusive. (PageID.967.) Gissantaner wrongly claims the sample should have been re-run, (PageID.766), as that part of the protocol does not apply to samples being analyzed with STRmix. Specifically, he cites to the part of the MSP policy that dictates how non-STRmix samples are to be developed. (*See* PageID.967 (suggesting oversaturated samples be run again as part of the general guidelines for

interpretation).) But the policy specifically authorizes the analysis to be transitioned to a qualified STRmix analyst where mixed-source interpretation is required. (PageID.970.) And during that STRmix analysis, the scientist is permitted to ignore peaks with identifiable artifacts (chemical snippets that register on the electropherogram but are not indicative of an allele), such as in oversaturation. (*See* PageID.995 ("[I]f a peak on the electropherogram is interpreted as arising from an artifact after considering the number of potential donors and the overall DNA profile, it may be removed from STRMix™ consideration during the IDx interpretation.").) Part of the rationale behind the MSP policy related to oversaturation is the detection limit of the instrumentation involved in capillary electrophoresis.

Given the designation of D8S1179 as inconclusive, the most reasonable interpretation of the electropherogram, and that provided by STRmix itself, is that the sample from the gun was that of a three-person mixture. Even so, the MSP is prepared to re-run the likelihood ratio calculation using a four-person (or other reasonable) assumption at Gissantaner's request, an offer that was made in writing on the lab report itself. He has not so requested, the government can only assume, because the resulting likelihood ratio will not be favorable to his case.

B. Probabilistic Genotyping, As Implemented by STRmix, Is Admissible Under the *Daubert* Factors

In sum, probabilistic genotyping in general, and STRmix in particular, are methods that are admissible under *Daubert*'s interpretation of Rules 701, 702, and 703. There is no legitimate dispute that determining the relative likelihood that Gissantaner's DNA was on the gun would assist the jury in determining whether he possessed it, as charged in the indictment. Likewise, it is clear that STRmix has been validated, both internally by laboratories and in peer-reviewed publications.

The *Daubert* factors are therefore readily satisfied. As cited above, several peer-reviewed publications discuss STRmix favorably. Forensic laboratories across the world have validated and adopted STRmix, and more are doing so each year, indicating STRmix passes the "testing" of which *Daubert* spoke. Even with the criticisms of the PCAST report, the authors of that report are cautiously optimistic about probabilistic genotyping and STRmix, which, combined with the peer-reviewed literature and wide adoption, is indicative of general acceptance. There is no readily describable "error rate" as such, but the likelihood ratio incorporates the animating principle behind that *Daubert* factor: it provides a mathematical description of the likelihood that the defendant's profile was found in the mixture by chance. And laboratories using STRmix, including the MSP, have lengthy, detailed standards governing the use of the software. (*E.g.*, PageID.978–99.)

Perhaps most importantly, STRmix has been internally validated by the MSP lab that used it, which should be sufficient on its own because internal validation hits two of the *Daubert* factors—testing and determination of error rate—in addition to being the touchstone of the "good grounds" about which the *Daubert* Court wrote.

Therefore, it is unsurprising that the state and federal courts that have reviewed STRmix have admitted it, with the only known exclusion based not on the program itself, but the absence of internal validation by the laboratory prior to its use. *Russell*, No. 1:14-cr-02563-MCA, slip op. at 18 ("STRMix has been tested for the purpose relevant here, . . . such tests have been peer-reviewed and published in scientific journals, and . . . its analyses are based on calculations recognized as reliable in the field."); *Pettway*, 2016 WL 6134493, at *2 ("Defendants may press their contentions concerning the longevity and reliability of STRmix on cross-examination and through their own expert witnesses. But nothing in their motion demonstrates that a Daubert

hearing or preclusion of evidence is necessary or warranted."); *Nelson v. State*, No. 02-16-00184-CR, 2017 WL 3526340 (Tex. Ct. App. Aug. 17, 2017) (affirming admission of STRmix evidence); *People v. Bullard-Daniel*, 54 Misc. 3d 177 (N.Y. Niagra Cnty. Ct. 2016) (admitting STRmix evidence); *see State v. Wakefield*, 9 N.Y.S. 3d 540 (N.Y. Sup. Ct. 2015) (admitting probabilistic genotyping evidence from TrueAllele, a competitor to STRmix); https://johnbuckleton.wordpress.com/strmix/ (last visited Feb. 14, 2018) (collecting slip opinions admitting STRmix); https://johnbuckleton.files.wordpress.com/2017/12/people-v-hillary-ii.pdf (last visited Feb, 14, 2018) (summarizing the scientific issues involved in *People v. Hillary*, a New York state case, in which the evidence was excluded).

C. The Defendant's Allegations Regarding the Handling of Evidence Are Premature and Do Not Bear on the *Daubert* Issue

The Court need not consider the issues raised by Gissantaner that relate to the BCPD's handling of evidence. Legally, all of the arguments are for the jury and do not implicate the *Daubert* gatekeeping function. Factually, the arguments require the Court to assume what the involved officers would testify to, something they will not do until the case is tried. Fundamentally, the arguments themselves are logically flawed and, whatever they insinuate about contamination, cannot explain why Gissantaner's DNA was on the gun.

1. Evidence Handling Is a Question of Weight and Not Admissibility

Putting aside, for a moment, Gissantaner's fraught speculation, all of his allegations relating to the chain of custody or the manner in which evidence was handled are for the jury. They go to weight, not admissibility, and should be the subject of defense counsel's cross examination of the officers involved. *See, e.g.*, *United States v. Knowles*, 623 F.3d 381, 386 (6th Cir. 2010); *United States v. Allen*, 619 F.3d 518, 525 (6th Cir. 2010) (citing *United States v.*

Allen, 106 F.3d 695, 700 (6th Cir. 1997)) ("Chain of custody issues are jury questions and the possibility of a break in the chain of custody of evidence goes to the weight of the evidence, not its admissibility."); *United States v. Combs*, 369 F.3d 925, 938 (6th Cir. 2004); *United States v. Levy*, 904 F.2d 1026, 1030 (6th Cir. 1990) ("[C]hallenges to the chain of custody go to the weight of evidence, not its admissibility.").

The Court does, through its gatekeeping function, have an obligation to keep from the jury evidence that has clearly been tampered with. "Physical evidence is admissible when the possibilities of misidentification or alteration are 'eliminated, not absolutely, but as a matter of reasonable probability.' *United States v. McFadden*, 458 F.2d 440, 441 (6th Cir.1972) (citation omitted). Merely raising the possibility of tampering is insufficient to render evidence inadmissible." *Allen*, 619 F.3d at 525. But Gissantaner has not met his burden of showing a reasonable probability of tampering, and his brief stops short of accusing the officers of tampering. Gissantaner does not cite a single case in which the types of chain-of-custody arguments he is making led to the exclusion of the evidence. Moreover, as discussed below, the allegations he makes do not undermine the relevant evidentiary conclusion—that Gissantaner's DNA is on the gun because he touched it.

2. The Defendant Assumes Too Much

Nor could Gissantaner meet his burden. The Federal Rules of Criminal Procedure do not provide for depositions absent "exceptional circumstances" not present here. Fed. R. Crim. P. 15(a)(1). Gissantaner will have to wait for trial to examine the officers on their recollection of the events of September 25, 2015. The reports and recordings disclosed to the defense summarize their expected testimony. In his brief, instead of hewing close to the facts recited in

those reports, Gissantaner speculates about what else the officers will testify to and insinuates misconduct where there is none.

Gissantaner's first critique of the BCPD is that one or two of the officers touched the gun before the evidence technician arrived to collect it. (PageID.773.) At the outset, police officers live in the real world, and while searching for evidence may occasionally come into contact with the contraband for which they were searching. In this case, the gun was found in a chest full of other belongings, and the officers' testimony at trial will establish if and why one or more of them touched the gun. Whatever their explanations, the DNA profile found on the gun is inconsistent with contamination by officers sloughing off and stirring up DNA. Gissantaner's claim to the contrary—that his DNA wound up on the gun because officers touched other items in the home, and then the gun—relies on the ideas of touch and transfer DNA.

As Gissantaner rightly points out, humans slough off skin cells every day, all day. Humans spit, sneeze, shed hair, and clip their nails. How many skin cells slough off, how much variation in DNA shedding exists among humans, and what the likelihood of transfer is, are all topics still subject to study. *See generally* C. Davies et al., *Assessing primary, secondary and tertiary DNA transfer using the Promega ESI-17 Fast PCR chemistry*, Forensic Science International: Genetics Supplement Series e55–57 (2015) (attached as Ex. 9) ("Unambiguous tertiary transfer was difficult to detect but cannot be ruled out."); Ane Elida Fonneløp et al., *Secondary and subsequent DNA transfer during criminal investigation*, 17 Forensic Science International: Genetics 155–62 (2015) (attached as Ex. 10) ("T]he risk of innocent DNA transfer at the crime-scene is currently not properly understood."). When two people shake hands, then, it is *possible* that Person A's DNA could be detected on a swab of Person B's palm. That is an example of primary transfer. When Person A touches Object B, which is then handled by Person

C, the detection of Person A's DNA on Person C is an example of secondary transfer. Gissantaner's theory is even more remote than that: he asserts there was tertiary transfer. He hypothesizes that because his DNA (Person A) was on objects in the home (Objects B), that officers searching the home (Persons C) not only picked up some of that DNA but then deposited it on the gun (Object D), before his DNA was found on the gun.

The problems with this hypothesis are multifold. First, while all agree that DNA can be and is transferred between people and objects, the frequency with which that occurs is unclear, though as observed by the Davies article, tertiary transfer is difficult to detect even under experimental conditions. Second, and relatedly, Gissantaner has offered no clue about what evidence will be introduced about DNA transfer at a *Daubert* hearing or at trial. Gissantaner's counsel's statements in the brief are not evidence, and while the brief alludes to an expert, it does not provide the summary required by Rule 16 of what that expert will say. On December 22, 2017, Gissantaner attempted to provide the Rule 16 notice. While that letter identified the topic of touch DNA, it did not summarize what the expert would say about it, or the bases for those opinions; moreover, that letter hedged on whether the defense expert would be called at all. (*Compare* Ex. 11 *with* Fed. R. Crim. P. 16(b)(1)(C) ("This summary must describe the witness's opinions, the bases and reasons for those opinions, and the witness's qualifications.").) The government objected to the lack of proper notice on December 28, 2017, but Gissantaner has not provided an amended notice. (*See* Ex. 12.) Short of Gissantaner properly noticing expected expert testimony in touch or transfer DNA, the government does not intend to call any witness to testify about it.

Third, the DNA profile on the gun is not consistent with Gissantaner's theory about DNA transfer. Gissantaner states that seven people lived in the home—two male adults, two female

adults, and three children of unspecified sex. (PageID.741.) At least five officers entered the home to search it, with at least three in the room with the gun. Therefore, under the theory where humans are sloughing off skin cells that are readily transferred to evidence, and counting only the officers who entered the room where the gun was found, at least *ten* individuals' DNA, including that from at least *five* males (Gissantaner, Patton, and the three searching officers, who were male), should have been found on the gun. Moreover, the facts as alleged by Gissantaner under his theory of the case, that the gun was Patton's—specifically that the gun was located in Patton's part of the house, and that male officers touched the gun prematurely—suggest that Patton's family's DNA and that of the officers should have been found on the gun. In fact, under his theory, it is much more likely that Patton's or the officers' DNA would have been found on the gun than Gissantaner's given that primary and secondary transfer are more probable than tertiary transfer.

That theory is inconsistent with the DNA analysis. Instead, as Gissantaner's brief indicates, the evidence suggests that the gun had on it the DNA of three people—Gissantaner, the female major contributor, and an additional minor contributor of undetermined sex. If the officers were shedding DNA and generally sloppy in handling the evidence, and if the gun belonged to Patton, why weren't multiple other male DNA profiles found on the weapon? Under the tertiary transfer theory, if the officers both picked up Gissantaner's DNA from other objects in the house and deposited it onto the gun, why didn't they also pick up DNA from the other residents of the house (in other words, why weren't there at least ten DNA profiles on the gun)?

Gissantaner does not have a theory that answers these questions, which is why he asks the Court to focus on the fact that an officer touched the gun while searching through a chest for evidence, and to overlook the insignificance of that touching. The hypothesis most consistent

with the evidence is that the DNA found on the gun was from the people who had handled it for a prolonged period, including Gissantaner.

Gissantaner's next criticism of the BCPD addresses the policies and procedures for transporting DNA evidence. Although the government produced the BCPD's documentation of the chain of custody, that, apparently, was not good enough for Gissantaner, who complains that "the discovery materials do not identify the methods by which the evidence was stored or transported" and accordingly "the government cannot demonstrate that the firearm was [not] ever in contact with any other individual or object." (PageID.774.) Gissantaner extrapolates that there was "[a] break in the chain of custody" because two entries on the custody log are separated by five days. (*Id.*) Gissantaner makes a throw-away argument about how two sticks used to swab Gissantaner's cheeks were not in the bag with the cotton swab residual after the samples were process by the lab. (PageID.776.)

This series of arguments is reckless speculation. The government will call the evidence technician at trial, who will testify about DNA collection in this case and in general.[8] BCPD is not required to have a written policy for every minute task conducted by officers, nor is it required to document the location of evidence on a continuous basis. It is sufficient to have well-trained officers who know how to properly collect and transport evidence, and to log the transfer of evidence from one secure location to another.

Gissantaner is wrong yet again when he looks to MSP's policies and procedures to throw shade at the BCPD. (PageID.775–76.) He makes two mistakes, one large and one small. First,

[8] Gissantaner accuses the evidence technician of misstating the time at which he collected Gissantaner's DNA in support of his argument that the BCPD is sloppy. (PageID.747 & n.3.) Gissantaner misreads the report: the report attached to Gissantaner's brief clearly states that the swabs were collected at 11:00 p.m., not 7:00 p.m. as Gissantaner claims. (PageID.791 ("Two . . . swabs collected via consent from DANIEL GISSANTANER . . . at 23:00 hours on 9/25/2015."); PageID.797 (chain of custody noting "Item Collected" at "09/25/2015 23:00").)

his broad criticism that BCPD does not have written guidelines for handling DNA evidence that are as detailed as the MSP's is misguided; a state laboratory is of course likely to be more focused on properly handling the large volume of samples it processes than is a local police department on how to collect evidence from a particular scene. There is a range of acceptable detail for written policies governing evidence collection, and every law enforcement agency is not required to have written manuals as detailed as the FBI's.

Second, Gissantaner says that the BCPD violated MSP policy by collecting his DNA; he was, after all, a convicted felon whose DNA profile was on file. (PageID.775.) The insinuation is that the supposedly improper collection of DNA from Gissantaner allowed for accidental cross contamination (at best), or intentional planting of evidence (at worst). But yet again, Gissantaner does not understand the manual he is citing, and he is reading an excerpt inapplicable to the facts of his case. The MSP laboratory has two separate DNA units—a CODIS unit (which administers the DNA profiling system, the rules for which are found in Gissantaner's Attachment 25), and a casework unit. The policy quoted in Gissantaner's brief applies to the CODIS unit. If a convicted felon is already in the CODIS database, when he is re-arrested his DNA is not recollected, because to do so would be a massive waste of resources: MSP would be entering felons into the CODIS database who were already there. By contrast, the casework unit *requires* DNA from a known suspect to be recollected and submitted for comparison. *See generally* FBI Laboratory, *National DNA Index System (NDS) Operational Procedures Manual, Version 6*, at 54 (effective July 17, 2017) (attached as Ex. 13) (describing how, even after a CODIS hit, a casework laboratory requires a "newly obtained known biological sample" for DNA analysis). A detailed discussion of the reasons for that policy is beyond the scope of this brief, but in short it has the benefit of efficiency (for example, DNA technologies change, and concurrent submission

of samples allows the samples to be run on the same platform), and statistical issues in interpretation (multiple hypothesis testing required by searching the CODIS database weakens the strength of the evidence). Here, too, Gissantaner is mistaken about the propriety of the analysis conducted in his case.

Finally, Gissantaner suggests sloppiness because the sticks from the buccal swabs collected from him were "not present" when counsel viewed the evidence. (PageID.749, 776.) But as Gissantaner acknowledges, the chain of custody shows the sticks are in BCPD's evidence. It appears that they were simply inadvertently not pulled for the evidence viewing, and they are available for Gissantaner's counsel to inspect.

IV. CONCLUSION

Gissantaner's litany of attacks on the DNA evidence in this case lack merit. Despite a 640-page submission, Gissantaner has no answer to the only reasonable explanation for the likelihood ratio of 49 million: that his DNA was on the gun. Gissantaner's criticisms are best explored through cross examination at trial. But these are not arguments that should keep this powerful and expertly developed forensic evidence from the jury.

Respectfully submitted,

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